Multiple Sclerosis (MS) Lesion Tracking Script

General Description

The Image Scripting functionality of MEDx was used to create a tool for the specific monitoring of the volume load of MS lesions over time. The script uses a 3D connected component analysis and a decoding algorithm for the longitudinal determination of the presence, the number, and the location of individual lesions (1). The sessions span over time. While processing each session, voxels belonging to a lesion are assigned a value of '2 to the power of session number'. The lesion mask images generated as such are then added. At the end of the analysis, the session contributions for each voxel are determined through a bitwise OR operation. Then through 3D connected component analysis lesions are assumed to be the same if they share a neighboring voxel or in the absence of neighboring voxels, if a third lesion links the two lesions together in 3D space.

To successfully run the script, open a New Folder. Go to **Toolbox**  **-> Volumetric** and select **MS Brain Lesion Analysis**. The tutorial provides an overview of the script to ensure its correct use and hence the reliability of the volume load measurements. The tutorial covers each GUI notebook page under a different subsection.

MS Brain Lesions GUI

Patient Info

The **Patient Info** page (Fig. 1) prompts the user for the patient directory and the type of acquisition.

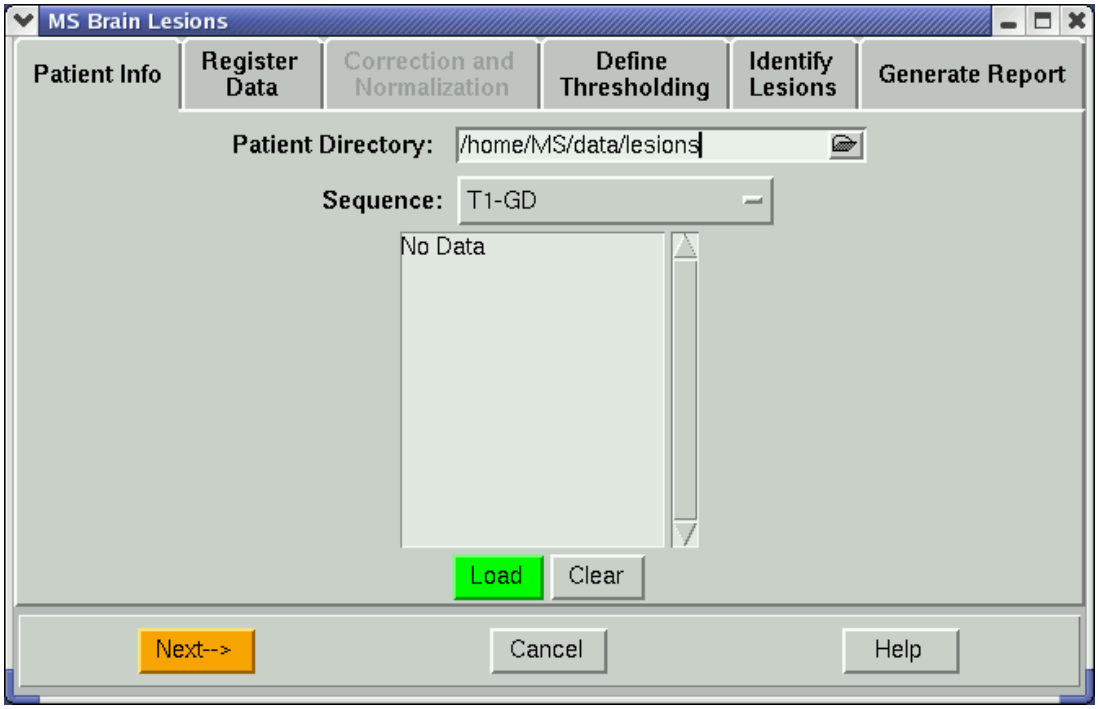


Fig.1. Patient Info page of the MS Brain Lesions GUI

Step 1: Click on the file folder icon across **Patient Directory** to specify the directory in which the results are to be stored. Clicking on the folder icon brings up the "Select A File" GUI. The directory should be specified across **Filter**. No specification is required under **Selection** since the required item is a directory.

Step 2: Press on the button across **Sequence** to see the acquisition options consisting of *T2*, *Flair*, *T1-BH*, *PD*, and *T1-Gd*. While *T1-BH* refers to T1 weighted acquisitions where the lesions appear as black holes, in *T1-Gd* acquisitions the lesions are enhanced.

Step 3: Now be sure to press on **Load**. The implication of the *No Data* message is that under the specified directory, the program has not been able to locate subdirectories with headings of t2, fl, t1, pd or gd. Each of these subdirectory headings respectively corresponds to the Sequence options listed in step 2.

Step 4: Press on **Next->** to proceed onto the **Register Data** page.

Register Data

This page provides options for registering the data or utilizing already registered data. The GUI for the two options differs in that when registration is required, the original images are loaded from hard disk; whereas in the case of the preregistered option, the images have to be in a MEDx folder whereby the Select button can be used to specify the images. The FSL Flirt algorithm is used for registration (see Chapter 34 of User's Guide). Figure 2 is the GUI page associated with this registration option.

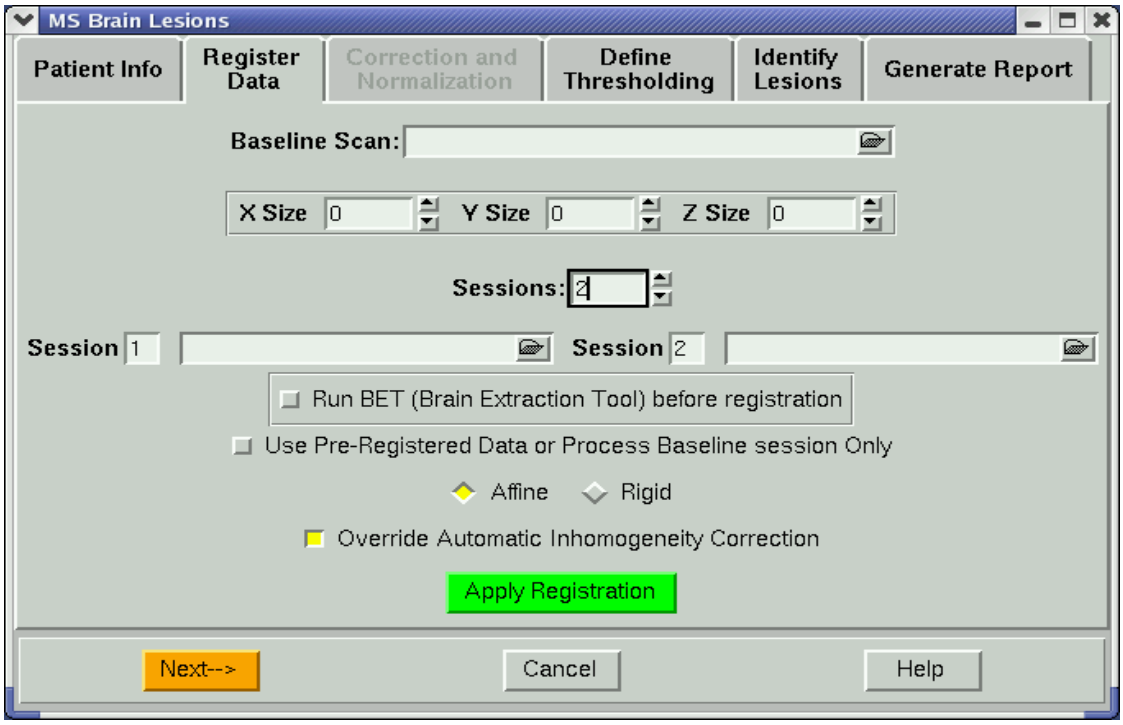


Fig.2. Register Data page when there is no Pre-Registered Data

Step 5: Across **Sessions** enter various numbers and observe how the GUI changes. Note that a maximum of 32 sessions is allowed.

Step 6: The default has been set to **Use Pre-Registered Data**. Note that the **X Size**, **Y Size**, and **Z Size** boxes are not there and the folder icons have been replaced by the **Select** buttons. For the case where registration is required, upon specification of the data, the X/Y/Z sizes are automatically calculated and loaded by the program.

Step 7: Specify the **Baseline Scan** as well as the data associated with the different Sessions. For now do not process more than 2 Sessions to conserve time. Sample data (e.g. ms0.hdr for Baseline and ms1.hdr for Session1) is available in $PXHOME/images/tutorials directory.

Step 8: Do not select **Run BET** as the registration is expected to be successful even without deskulling.

Step 9: The default has been set to **Override Automatic Inhomogeneity Correction**. Without inhomogeneity correction, the user should still be able to identify the lesions.

Step 10: If you are in **Use Pre-Registered** option, be sure to press on **Load Data**. Otherwise, you must be registering your data. So press on **Apply Registration**.

Step 11: When you are through with this page, press on **Next->**.

Correction and Normalization

To normalize the data, across **Image Volume**, any of the *Baseline* or *Session* images can be specified whereby upon pressing on **Apply**, the program proceeds with normalization. For now press on **Next->** to proceed to the **Define Thresholding** page.

Define Thresholding

The purpose of this page is to determine the proper threshold. So not all lesions within the volume have to be traced. The threshold can be determined by tracing one lesion.

Step 12: Across **Image Volume**, press on the **Select** button to specify the Baseline or one of the Session images.

Step 13: For **Graphic Type**, select *Free Hand*. Then press on **Place Graphic**. A Script Pause message will appear instructing you to *Please free-hand draw region, then select OK*. Draw a rough outline of one lesion.

Step 14: Specify a **Low Threshold** and a **High Threshold**. Be sure to press on **Assign Threshold to Slice** or **Assign Threshold to All**; then select **Toggle White**. With **Assign Threshold to Slice**, the threshold is applicable only to the current slice. With **Assign Threshold to All**, the threshold becomes applicable to all regions regardless of slice. If the thresholds were properly chosen, upon pressing on **Toggle White**, the lesion should have appeared as white.

Step 15: If the lesion is not properly selected, first deselect **Toggle White** to go back to the original image. Then press on **Delete Graphics** and return to Step 12.

Step 16: If the lesion is properly selected, after deselecting **Toggle White**, you can proceed to **Identify Lesions** page by pressing on **Next**.

Identify Lesions

Identifying the lesions can be tedious as the contour of each lesion has to be traced manually. The tracing does not have to be exact provided the lesion is fully included. The specified thresholds then accurately identify the lesion within the specified region.

Step 17: Across **Image Volume**, press on the **Select** button to specify the Baseline or one of the Session images.

Step 18: Select the **Graphic Type** and if you want to specify additional lesions, press on **Place Graphic**. For the *Rectangle* or *Ellipse* options, the graphic has to be adjusted to make sure it includes the lesion. Alternately if you already have ROI templates, you can load them by selecting the **Use Previously Created ROI Template** option.

Step 19: Press on **Toggle White** as a cautionary measure to see if the specified thresholds correctly identified the lesion. Only the lesions identified by **Toggle White** will be included in the computation. To go back to the original image, you have to deselect **Toggle White**.

Step 20: After identifying all of the lesions, press on **Compute**. Note that you have to press on **Compute** after processing each Image Volume i.e. after processing Baseline; then after processing on Session1 etc.

Step 21: Now press on **Next->** to proceed to the **Generate Report** page.

Generate Report

The final page provides options for viewing the lesions and generating a summary report. Figure 3 is the GUI for the final page for the **View Lesions** option.

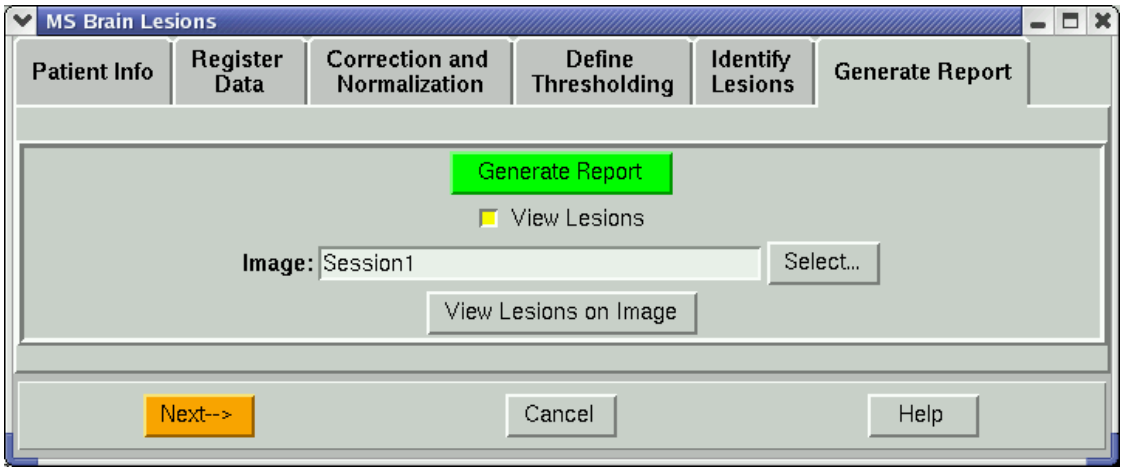
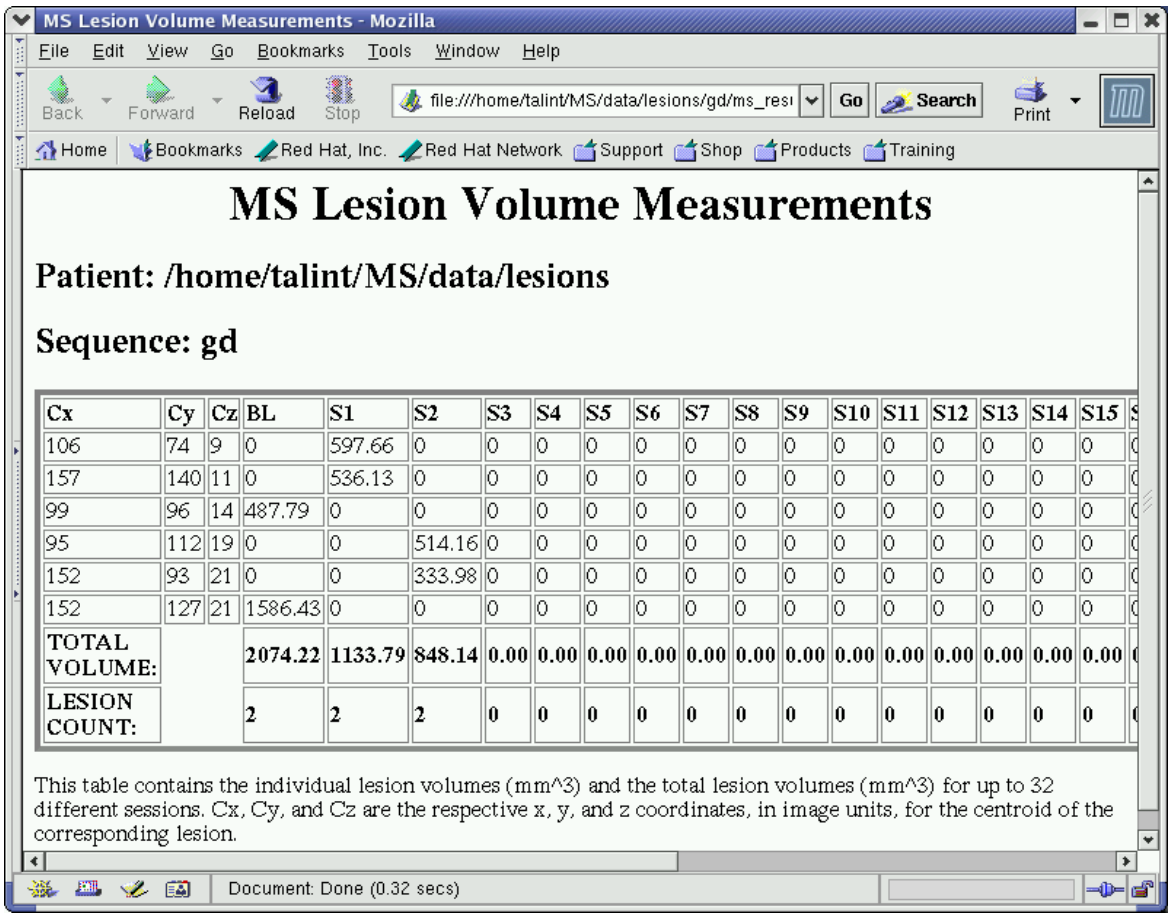


Figure 3. Generate Report page for the View Lesions option

Step 22: If you want to double check prior to generating the report, select the **View Lesions** option. Across **Image** select the session you are interested in. Then press on **View Lesions on Image**. The lesions associated with that particular session will be superimposed in yellow onto the brain. The lesions on the *Baseline* and other *Session*s can be checked similarly.

Step 23: Deselect the **View Lesions** option. The **Image** entry and **View Lesions on Image** button are no longer visible. From the Page Manager go to the Session1 page or to Baseline. Select the **View All Lesions** option. Lesions from all sessions will now be superimposed on the brain.

Step 24: Assuming you are happy with the lesion depictions, press on **Generate Report**. A summary of the lesion locations, volumes along with the session in which they were recorded will appear in the table. A sample report is provided below. In Fig. 4, only a subsection of the report appears due to space constraints.



Cx	Cy	Cz	BL	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13	S14	S15
106	74	9	0	597.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0
157	140	11	0	536.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0
99	96	14	487.79	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
95	112	19	0	0	514.16	0	0	0	0	0	0	0	0	0	0	0	0	0
152	93	21	0	0	333.98	0	0	0	0	0	0	0	0	0	0	0	0	0
152	127	21	1586.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TOTAL VOLUME:			**2074.22**	**1133.79**	**848.14**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**	**0.00**
LESION COUNT:			**2**	**2**	**2**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**

This table contains the individual lesion volumes (mm^3) and the total lesion volumes (mm^3) for up to 32 different sessions. Cx, Cy, and Cz are the respective x, y, and z coordinates, in image units, for the centroid of the corresponding lesion.

Figure 4. Generate Report page for the View Lesions option

CONGRATULATIONS!! You are now ready to proceed with an analysis of your own.

References

Gupta S, Solomon JM, Tasciyan TA, Cao MM, Stone RD, Ostuni JL, Chayon JM, Muraro PA, Frank JA, Richert ND, McFarland HF, Bagnato F. “Interferon-beta-1b

effects on re-enhancing lesions in patients with multiple sclerosis," Multiple Sclerosis (in print).